



SEQUENCE LISTING

<110> Kevin Baker et al.

<120> HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR16

<130> PF514P1

<150> 60/268,364

<151> 2001-02-14

<150> 09/637,856

<151> 2000-08-10

<150> 60/148,348

<151> 1999-08-12

<150> 60/148,683

<151> 1999-08-13

<150> 60/148,758

<151> 1999-08-16

<150> 60/148,870

<151> 1999-08-13

<150> 60/149,181

<151> 1999-08-17

<150> 60/149,453

<151> 1999-08-18

<150> 60/149,498

<151> 1999-08-18

<160> 43

<170> PatentIn version 3.0

<210> 1

<211> 3390

<212> DNA

<213> human

<400> 1

atgctgttcc ggcggcgagg gccggtacgg ggcaggggct gggggcgggc ggcggaggct
60

ccccgccgcg ggcgctcgcc gccctggagc cccgcctgga tttgctgctg ggcgctcgcc
120

ggctgccagg cggcctgggc tggggacctg cctcctcct ccagccgccc gcttcctcct
180

tgccaggaga aagattatca ctttgaatat acggaatgtg atagcagtgg ctccagggtgg
240

agagttgcca ttccaaattc tgcagtggac tgctctggcc tgcttgaccc agtgagaggc
300

aaagaatgca ctttctcctg tgcttctgga gagtatctag aaatgaagaa ccagggtatgc
360

agtaagtgtg gtgaaggcac ctattccttg ggcagtggca tcaaatttga tgaatgggat
420

gaattgccgg caggattttc taacatcgca acattcatgg aactgtggt gggcccttct
480

gacagcaggc cagacggctg taacaactct tcttgatcc ctctggaaa ctacatagaa
540

tctaactcgtg atgactgcac ggtgtctttg atctatgctg tgcaccttaa gaagtcaggc
600

tatgtcttct ttgagtacca gtatgtcgac aacaacatct tctttgagtt ctttattcaa
660

aatgatcagt gccaggagat ggacaccacc actgacaagt gggtaaaact tacagacaat
720

ggagaatggg gctctcattc tgtaatgctg aaatcaggca caaacatact ctactggaga
780

actacaggca tccttatggg ttctaaggcg gtcaagcctg tgctggtaaa aaatatcaca
840

attgaagggg tggcgtacac atcagaatgt tttccttgca agccaggcac attcagcaac
900

aaaccagggt cattcaactg ccagggtgtg cccagaaaca cctattctga gaaaggagcc
960

aaagaatgta taagggtgtaa agacgactct caattttcag gatccagtga gtgtacagag
1020

cgccctccct gtaccacaaa agactatttc cagatccata ctccatgtga tgaagaagga
1080

aagacacaga taatgtacaa gtggatagag cccaaaatct gccgggagga tctcacagat
1140

gctattagat tgcccccttc tggagagaag aaggattgtc cgccttgcaa ccctggattt
1200

tataacaatg gatcatcttc ttgccatccc tgtcctcctg gaacattttc agatggaacc
1260

aaagaatgta gaccatgtcc agcaggaacg gagcctgcac ttggctttga atataaatgg
1320

tggaatgtcc ttcctggcaa catgaaaact tcctgcttca atgttgggaa ttcaaagtgc
1380

gatggaatga atggttggga ggtggctgga gatcatatcc agagtggggc tggaggttct
1440

gacaatgatt acctgatctt aaacttgcac atcccaggat ttaaaccacc aacatctatg
1500

actggagcca cgggttctga actaggaaga ataacatttg tctttgagac cctctgttca
1560

gctgactgtg ttttgtactt catggtggat attaatagaa aaagtacaaa tgtggtagaa
1620

tcgtgggggtg gaaccaaaga aaaacaagct tacacccata tcattcttcaa gaatgcaact
1680

tttacattta catgggcatt ccagagaact aatcagggtc aagataatag acggttcac
1740

aatgacatgg tgaagattta ttctatcaca gccactaatg cagttgatgg ggtggcgtcc
1800

tcatgccgtg cctgtgccct cggttctgaa cagtcggggt catcgtgtgt ccctgccct
1860

ccaggccact acattgagaa agaaaccaac cagtgcagg aatgtccacc tgacacctac
1920

ctgtccatac atcagggtcta tggcaaagag gcttgtattc catgcgggcc tgggagtaaa
1980

aacaatcagg accattcggg ttgctatagt gactgctttt tctaccatga aaaagaaaat
2040

cagattttgc actatgactt tagcaacctc agcagtgtgg gctcattaat gaatggcccc
2100

agcttcacct ccaaaggaac aaaatacttc catttcttca atatcagttt atgtggggcat
2160

gaggggaaga agatggctct ctgtaccaac aatataacag actttacagt aaaagaaata
2220

gtggcagggg cagatgatta cacaaatttg gtagggggcat ttgtatgcca gtcaacaatt
2280

attccttctg aaagtaaggg tttccgagca gccttatcat cacaatccat cattctggca
2340

gatacattca taggagtcac agttgaaacc acattgaaaa atattaatat aaaagaagat
2400

atgttcccag ttccaacaag ccaaatacca gatgtgcatt tcttttataa gtcttctaca
2460

gcaacaacat cttgtattaa tggccgatca actgctgtga aaatgaggtg taatcctact
2520

aaatctggag caggagtgat ttcagtcccc agcaagtgcc cagcagggtac ctgtgatggg
2580

tgtacgttct atttcctgtg ggagagtgtg gaagcttgcc ctctgtgtac ggagcatgac
2640

ttccatgaga ttgaggggagc ctgcaagaga ggatttcagg aaaccttgta tgtgtggaat
2700

gaacctaaat ggtgcattaa aggaatttct ttgcctgaga aaaagttggc aacctgtgaa
2760

acggttgact tttggctgaa ggtgggagcc ggtgtgggag cttttactgc cgttttgctg
2820

gtggctctga cctgctactt ctggaaaaag aatcaaaaaga aaaagaagac cattttgaat
2880

ctgttcaact gaaaacctca agatccccaa atatatgaag agacagtgtg gtagccttga
2940

gactaatgaa caaagaaacc tgctctagtt ttacaggacc atatttttagg gtctgtcctc
3000

atacctgtca cattgggtgat ctcacagagg agggccatgc cgctgaaaag ggaaggagat
3060

tgaaacattt gattgcctta tcacatgggtc aagtaccttg ccaaataaag gaaagcaaatt
3120

gatttgggtc tcaactgaag atgaagctca actcaggaag agatttatct gtatatcac
3180

ataactgaaa accaagttta agcccaccaa tgcactgctg atgcatgccca tataattaat
3240

gggtaacttt tattctttat gatgtctaca taacaagtgt gatttggaag gcacatgtga
3300

gcatatgcat tatgatccaa tttatgtttt ttctttgttt atattttggg gaaaattaa
3360

atttttttaa ggtaaaaaaaaa aaaaaaaaaa
3390

<210> 2
<211> 963
<212> PRT
<213> human

<400> 2

Met Leu Phe Arg Ala Arg Gly Pro Val Arg Gly Arg Gly Trp Gly Arg
1 5 10 15

Pro Ala Glu Ala Pro Arg Arg Gly Arg Ser Pro Pro Trp Ser Pro Ala
20 25 30

Trp Ile Cys Cys Trp Ala Leu Ala Gly Cys Gln Ala Ala Trp Ala Gly
35 40 45

Asp Leu Pro Ser Ser Ser Ser Arg Pro Leu Pro Pro Cys Gln Glu Lys
50 55 60

Asp Tyr His Phe Glu Tyr Thr Glu Cys Asp Ser Ser Gly Ser Arg Trp
65 70 75 80

Arg Val Ala Ile Pro Asn Ser Ala Val Asp Cys Ser Gly Leu Pro Asp

85								90				95			
Pro	Val	Arg	Gly 100	Lys	Glu	Cys	Thr	Phe 105	Ser	Cys	Ala	Ser	Gly 110	Glu	Tyr
Leu	Glu	Met 115	Lys	Asn	Gln	Val	Cys 120	Ser	Lys	Cys	Gly	Glu 125	Gly	Thr	Tyr
Ser	Leu 130	Gly	Ser	Gly	Ile	Lys 135	Phe	Asp	Glu	Trp	Asp 140	Glu	Leu	Pro	Ala
Gly 145	Phe	Ser	Asn	Ile	Ala 150	Thr	Phe	Met	Asp	Thr 155	Val	Val	Gly	Pro	Ser 160
Asp	Ser	Arg	Pro	Asp 165	Gly	Cys	Asn	Asn	Ser 170	Ser	Trp	Ile	Pro	Arg	Gly 175
Asn	Tyr	Ile	Glu 180	Ser	Asn	Arg	Asp	Asp 185	Cys	Thr	Val	Ser	Leu 190	Ile	Tyr
Ala	Val	His 195	Leu	Lys	Lys	Ser	Gly 200	Tyr	Val	Phe	Phe	Glu 205	Tyr	Gln	Tyr
Val	Asp 210	Asn	Asn	Ile	Phe	Phe 215	Glu	Phe	Phe	Ile	Gln 220	Asn	Asp	Gln	Cys
Gln 225	Glu	Met	Asp	Thr	Thr 230	Thr	Asp	Lys	Trp	Val 235	Lys	Leu	Thr	Asp	Asn 240
Gly	Glu	Trp	Gly	Ser 245	His	Ser	Val	Met	Leu 250	Lys	Ser	Gly	Thr	Asn 255	Ile
Leu	Tyr	Trp	Arg 260	Thr	Thr	Gly	Ile	Leu 265	Met	Gly	Ser	Lys	Ala 270	Val	Lys
Pro	Val	Leu 275	Val	Lys	Asn	Ile	Thr 280	Ile	Glu	Gly	Val	Ala 285	Tyr	Thr	Ser
Glu	Cys 290	Phe	Pro	Cys	Lys	Pro 295	Gly	Thr	Phe	Ser	Asn 300	Lys	Pro	Gly	Ser
Phe 305	Asn	Cys	Gln	Val	Cys 310	Pro	Arg	Asn	Thr	Tyr 315	Ser	Glu	Lys	Gly	Ala 320
Lys	Glu	Cys	Ile	Arg 325	Cys	Lys	Asp	Asp	Ser 330	Gln	Phe	Ser	Gly	Ser 335	Ser
Glu	Cys	Thr	Glu	Arg	Pro	Pro	Cys	Thr	Thr	Lys	Asp	Tyr	Phe	Gln	Ile

340					345					350					
His	Thr	Pro	Cys	Asp	Glu	Glu	Gly	Lys	Thr	Gln	Ile	Met	Tyr	Lys	Trp
		355					360					365			
Ile	Glu	Pro	Lys	Ile	Cys	Arg	Glu	Asp	Leu	Thr	Asp	Ala	Ile	Arg	Leu
	370					375					380				
Pro	Pro	Ser	Gly	Glu	Lys	Lys	Asp	Cys	Pro	Pro	Cys	Asn	Pro	Gly	Phe
385					390					395					400
Tyr	Asn	Asn	Gly	Ser	Ser	Ser	Cys	His	Pro	Cys	Pro	Pro	Gly	Thr	Phe
				405					410					415	
Ser	Asp	Gly	Thr	Lys	Glu	Cys	Arg	Pro	Cys	Pro	Ala	Gly	Thr	Glu	Pro
			420					425					430		
Ala	Leu	Gly	Phe	Glu	Tyr	Lys	Trp	Trp	Asn	Val	Leu	Pro	Gly	Asn	Met
		435					440					445			
Lys	Thr	Ser	Cys	Phe	Asn	Val	Gly	Asn	Ser	Lys	Cys	Asp	Gly	Met	Asn
	450					455					460				
Gly	Trp	Glu	Val	Ala	Gly	Asp	His	Ile	Gln	Ser	Gly	Ala	Gly	Gly	Ser
465					470					475					480
Asp	Asn	Asp	Tyr	Leu	Ile	Leu	Asn	Leu	His	Ile	Pro	Gly	Phe	Lys	Pro
				485					490					495	
Pro	Thr	Ser	Met	Thr	Gly	Ala	Thr	Gly	Ser	Glu	Leu	Gly	Arg	Ile	Thr
			500					505					510		
Phe	Val	Phe	Glu	Thr	Leu	Cys	Ser	Ala	Asp	Cys	Val	Leu	Tyr	Phe	Met
		515					520					525			
Val	Asp	Ile	Asn	Arg	Lys	Ser	Thr	Asn	Val	Val	Glu	Ser	Trp	Gly	Gly
	530					535					540				
Thr	Lys	Glu	Lys	Gln	Ala	Tyr	Thr	His	Ile	Ile	Phe	Lys	Asn	Ala	Thr
545					550					555					560
Phe	Thr	Phe	Thr	Trp	Ala	Phe	Gln	Arg	Thr	Asn	Gln	Gly	Gln	Asp	Asn
				565					570					575	
Arg	Arg	Phe	Ile	Asn	Asp	Met	Val	Lys	Ile	Tyr	Ser	Ile	Thr	Ala	Thr
			580					585					590		
Asn	Ala	Val	Asp	Gly	Val	Ala	Ser	Ser	Cys	Arg	Ala	Cys	Ala	Leu	Gly

595					600					605					
Ser	Glu	Gln	Ser	Gly	Ser	Ser	Cys	Val	Pro	Cys	Pro	Pro	Gly	His	Tyr
	610					615					620				
Ile	Glu	Lys	Glu	Thr	Asn	Gln	Cys	Lys	Glu	Cys	Pro	Pro	Asp	Thr	Tyr
625					630					635					640
Leu	Ser	Ile	His	Gln	Val	Tyr	Gly	Lys	Glu	Ala	Cys	Ile	Pro	Cys	Gly
				645					650					655	
Pro	Gly	Ser	Lys	Asn	Asn	Gln	Asp	His	Ser	Val	Cys	Tyr	Ser	Asp	Cys
			660					665					670		
Phe	Phe	Tyr	His	Glu	Lys	Glu	Asn	Gln	Ile	Leu	His	Tyr	Asp	Phe	Ser
		675					680					685			
Asn	Leu	Ser	Ser	Val	Gly	Ser	Leu	Met	Asn	Gly	Pro	Ser	Phe	Thr	Ser
	690					695					700				
Lys	Gly	Thr	Lys	Tyr	Phe	His	Phe	Phe	Asn	Ile	Ser	Leu	Cys	Gly	His
705					710					715					720
Glu	Gly	Lys	Lys	Met	Ala	Leu	Cys	Thr	Asn	Asn	Ile	Thr	Asp	Phe	Thr
				725					730					735	
Val	Lys	Glu	Ile	Val	Ala	Gly	Ser	Asp	Asp	Tyr	Thr	Asn	Leu	Val	Gly
			740					745					750		
Ala	Phe	Val	Cys	Gln	Ser	Thr	Ile	Ile	Pro	Ser	Glu	Ser	Lys	Gly	Phe
		755					760					765			
Arg	Ala	Ala	Leu	Ser	Ser	Gln	Ser	Ile	Ile	Leu	Ala	Asp	Thr	Phe	Ile
	770					775					780				
Gly	Val	Thr	Val	Glu	Thr	Thr	Leu	Lys	Asn	Ile	Asn	Ile	Lys	Glu	Asp
785					790					795					800
Met	Phe	Pro	Val	Pro	Thr	Ser	Gln	Ile	Pro	Asp	Val	His	Phe	Phe	Tyr
				805					810					815	
Lys	Ser	Ser	Thr	Ala	Thr	Thr	Ser	Cys	Ile	Asn	Gly	Arg	Ser	Thr	Ala
			820					825					830		
Val	Lys	Met	Arg	Cys	Asn	Pro	Thr	Lys	Ser	Gly	Ala	Gly	Val	Ile	Ser
		835					840					845			
Val	Pro	Ser	Lys	Cys	Pro	Ala	Gly	Thr	Cys	Asp	Gly	Cys	Thr	Phe	Tyr

850					855					860					
Phe	Leu	Trp	Glu	Ser	Ala	Glu	Ala	Cys	Pro	Leu	Cys	Thr	Glu	His	Asp
865					870					875					880
Phe	His	Glu	Ile	Glu	Gly	Ala	Cys	Lys	Arg	Gly	Phe	Gln	Glu	Thr	Leu
				885					890					895	
Tyr	Val	Trp	Asn	Glu	Pro	Lys	Trp	Cys	Ile	Lys	Gly	Ile	Ser	Leu	Pro
			900					905					910		
Glu	Lys	Lys	Leu	Ala	Thr	Cys	Glu	Thr	Val	Asp	Phe	Trp	Leu	Lys	Val
		915					920					925			
Gly	Ala	Gly	Val	Gly	Ala	Phe	Thr	Ala	Val	Leu	Leu	Val	Ala	Leu	Thr
	930					935					940				
Cys	Tyr	Phe	Trp	Lys	Lys	Asn	Gln	Lys	Lys	Lys	Lys	Thr	Ile	Leu	Asn
945					950					955					960

Leu Phe Asn

<210> 3
 <211> 3556
 <212> DNA
 <213> human

<400> 3
 atgctgttcc gcgcccgggg gccggtacgg ggcaggggct gggggcggcc ggcggaggct
 60
 ccccgccgcg ggcgctcgcc gccctggagc cccgcctgga tttgctgctg ggcgctcgcc
 120
 ggctgccagg cggcctgggc tggggacctg ccctcctcct ccagccgccc gcttcctcct
 180
 tgccaggaga aagattatca ctttgaatat acggaatgtg atagcagtgg ctccagggtg
 240
 agagttgcca ttccaaattc tgcagtggac tgctctggcc tgccctgaccc agtgagaggc
 300
 aaagaatgca ctttctcctg tgcttctgga gagtatctag aaatgaagaa ccagggtatgc
 360
 agtaagtgtg gtgaaggcac ctattccttg ggcagtggca tcaaatttga tgaatgggat

420

gaattgccgg caggattttc taacatcgca acattcatgg acactgtggt gggcccttct
480

gacagcaggc cagacggctg taacaactct tcttgatcc ctcgtggaaa ctacatagaa
540

tctaatacgtg atgactgcac ggtgtctttg atctatgctg tgcaccttaa gaagtcaggc
600

tatgtcttct ttgagtacca gtatgtcgac aacaacatct tctttgagtt ctttattcaa
660

aatgatcagt gccaggagat ggacaccacc actgacaagt gggtaaaact tacagacaat
720

ggagaatggg gctctcattc tgtaatgctg aaatcaggca caaacatact ctactggaga
780

actacaggca tccttatggg ttctaaggcg gtcaagcctg tgctggtaaa aaatatcaca
840

attgaagggg tggcgtacac atcagaatgt tttccttgca agccaggcac attcagcaac
900

aaaccagggt cattcaactg ccagggtgtg cccagaaaca cctattctga gaaaggagcc
960

aaagaatgta taagggtgtaa agacgactct caattttcag gatccagtga gtgtacagag
1020

cgccctccct gtaccacaaa agactatttc cagatccata ctccatgtga tgaagaagga
1080

aagacacaga taatgtacaa gtggatagag cccaaaatct gccgggagga tctcacagat
1140

gctattagat tgcccccttc tggagagaag aaggattgtc cgccttgcaa ccctggattt
1200

tataacaatg gatcatcttc ttgccatccc tgtcctcctg gaacattttc agatggaacc
1260

aaagaatgta gaccatgtcc agcaggaacg gagcctgcac ttggctttga atataaatgg
1320

tggaatgtcc ttcctggcaa catgaaaact tcctgcttca atgttgggaa ttcaaagtgc

1380

gatggaatga atgggttggga ggtggctgga gatcatatcc agagtggggc tggagggttct
1440

gacaatgatt acctgatctt aaacttgcatt atcccaggat ttaaaccacc aacatctatg
1500

actggagcca cgggttctga actaggaaga ataacatttg tctttgagac cctctgttca
1560

gctgactgtg ttttgtactt catgggtggat attaatagaa aaagtacaaa tgtggtagaa
1620

tcgtgggggtg gaaccaaaga aaaacaagct tacacccata tcattcttcaa gaatgcaact
1680

tttacattta catgggcatt ccagagaact aatcagggtc aagataatag acggttcatt
1740

aatgacatgg tgaagattta ttctatcaca gccactaatg cagttgatgg ggtggcgctc
1800

tcattgccgtg cctgtgccct cggttctgaa cagtcggggt catcgtgtgt cccctgccct
1860

ccaggccact acattgagaa agaaaccaac cagtgcagg aatgtccacc tgacacctac
1920

ctgtccatac atcagggtcta tggcaaagag gcttgtattc catgcggggc tgggagtaaa
1980

aacaatcagg accattcggg ttgctatagt gactgctttt tctaccatga aaaagaaaat
2040

cagattttgc actatgactt tagcaacctc agcagtgtgg gctcattaat gaatggcccc
2100

agcttcacct ccaaaggaac aaaatacttc catttcttca atatcagttt atgtgggcat
2160

gaggggaaga agatggctct ctgtaccaac aatataacag actttacagt aaaagaaata
2220

gtggcagggt cagatgatta cacaatttg gtaggggcat ttgtatgcca gtcaacaatt
2280

attccttctg aaagtaaggg tttccgagca gccttatcat cacaatccat cattctggca

2340

gatacattca taggagtcac agttgaaacc acattgaaaa atattaatat aaaagaagat
2400

atgttcccag ttccaacaag ccaaatacca gatgtgcatt tctttttataa gtcttctaca
2460

gcaacaacat cttgtattaa tggccgatca actgctgtga aaatgagggtg taatcctact
2520

aaatctggag caggagtgat ttcagtcacc agcaagtgcc cagcagggtac ctgtgatggg
2580

tgtacgttct atttcctgtg ggagagtgct gaagcttgcc ctctgtgtac ggagcatgac
2640

ttccatgaga ttgagggagc ctgcaagaga ggatttcagg aaaccttgta tgtgtggaat
2700

gaacctaaat ggtgcattaa aggaatttct ttgcctgaga aaaagttggc aacctgtgaa
2760

acggttgact tttggctgaa ggtgggagcc ggtgtgggag cttttactgc cgttttgctg
2820

gtggctctga cctgctactt ctggaaaaag aatcaaaaac tggaatacaa atattccaag
2880

ttagtaatga cgactaactc aaaagagtgt gaactcccgg ctgcagacag ttgtgctatc
2940

atggaaggag aagataatga agaggaagtt gtatatcca ataaacagtc actactagga
3000

aaactcaaat ctttggcaac caaggaaaaa gaagaccatt ttgaatctgt tcaactgaaa
3060

acctcaagat ccccaaatat atgaagagac agtgctgtag ccttgagact aatgaacaaa
3120

gaaacctgct ctagttttac aggaccatat tttaggggtct gtcctcatac ctgtcacatt
3180

ggtgatctca cagaggaggg ccatgccgct gaaaaggga ggagattgaa acatttgatt
3240

gccttatcac atggtcaagt accttgccaa ataaaggaaa gcaaatgatt tgggtctcaa

3300

ctgaagatga agctcaactc aggaagagat ttatctgtat atacacataa ctgaaaacca
3360

agtttaagcc caccaatgca ctgctgatgc atgccatata attaatgggt aactttttatt
3420

ctttatgatg tctacataac aagtgtgatt tggaaggcac atgtgagcat atgcattatg
3480

atccaattta tgtttttttct ttgtttatat tttggggaaa attaaaattt ttttaaggta
3540

aaaaaaaaaa aaaaaa
3556

<210> 4
<211> 1027
<212> PRT
<213> human

<400> 4

Met Leu Phe Arg Ala Arg Gly Pro Val Arg Gly Arg Gly Trp Gly Arg
1 5 10 15

Pro Ala Glu Ala Pro Arg Arg Gly Arg Ser Pro Pro Trp Ser Pro Ala
20 25 30

Trp Ile Cys Cys Trp Ala Leu Ala Gly Cys Gln Ala Ala Trp Ala Gly
35 40 45

Asp Leu Pro Ser Ser Ser Ser Arg Pro Leu Pro Pro Cys Gln Glu Lys
50 55 60

Asp Tyr His Phe Glu Tyr Thr Glu Cys Asp Ser Ser Gly Ser Arg Trp
65 70 75 80

Arg Val Ala Ile Pro Asn Ser Ala Val Asp Cys Ser Gly Leu Pro Asp
85 90 95

Pro Val Arg Gly Lys Glu Cys Thr Phe Ser Cys Ala Ser Gly Glu Tyr
100 105 110

Leu Glu Met Lys Asn Gln Val Cys Ser Lys Cys Gly Glu Gly Thr Tyr
115 120 125

Ser	Leu	Gly	Ser	Gly	Ile	Lys	Phe	Asp	Glu	Trp	Asp	Glu	Leu	Pro	Ala
130						135					140				
Gly	Phe	Ser	Asn	Ile	Ala	Thr	Phe	Met	Asp	Thr	Val	Val	Gly	Pro	Ser
145					150					155					160
Asp	Ser	Arg	Pro	Asp	Gly	Cys	Asn	Asn	Ser	Ser	Trp	Ile	Pro	Arg	Gly
				165					170					175	
Asn	Tyr	Ile	Glu	Ser	Asn	Arg	Asp	Asp	Cys	Thr	Val	Ser	Leu	Ile	Tyr
			180					185					190		
Ala	Val	His	Leu	Lys	Lys	Ser	Gly	Tyr	Val	Phe	Phe	Glu	Tyr	Gln	Tyr
		195					200					205			
Val	Asp	Asn	Asn	Ile	Phe	Phe	Glu	Phe	Phe	Ile	Gln	Asn	Asp	Gln	Cys
	210					215					220				
Gln	Glu	Met	Asp	Thr	Thr	Thr	Asp	Lys	Trp	Val	Lys	Leu	Thr	Asp	Asn
225					230					235					240
Gly	Glu	Trp	Gly	Ser	His	Ser	Val	Met	Leu	Lys	Ser	Gly	Thr	Asn	Ile
				245					250					255	
Leu	Tyr	Trp	Arg	Thr	Thr	Gly	Ile	Leu	Met	Gly	Ser	Lys	Ala	Val	Lys
			260					265					270		
Pro	Val	Leu	Val	Lys	Asn	Ile	Thr	Ile	Glu	Gly	Val	Ala	Tyr	Thr	Ser
		275					280					285			
Glu	Cys	Phe	Pro	Cys	Lys	Pro	Gly	Thr	Phe	Ser	Asn	Lys	Pro	Gly	Ser
	290					295					300				
Phe	Asn	Cys	Gln	Val	Cys	Pro	Arg	Asn	Thr	Tyr	Ser	Glu	Lys	Gly	Ala
305					310					315					320
Lys	Glu	Cys	Ile	Arg	Cys	Lys	Asp	Asp	Ser	Gln	Phe	Ser	Gly	Ser	Ser
				325					330					335	
Glu	Cys	Thr	Glu	Arg	Pro	Pro	Cys	Thr	Thr	Lys	Asp	Tyr	Phe	Gln	Ile
			340					345					350		
His	Thr	Pro	Cys	Asp	Glu	Glu	Gly	Lys	Thr	Gln	Ile	Met	Tyr	Lys	Trp
		355					360					365			
Ile	Glu	Pro	Lys	Ile	Cys	Arg	Glu	Asp	Leu	Thr	Asp	Ala	Ile	Arg	Leu
	370					375					380				

Pro 385	Pro	Ser	Gly	Glu	Lys 390	Lys	Asp	Cys	Pro	Pro 395	Cys	Asn	Pro	Gly	Phe 400
Tyr	Asn	Asn	Gly	Ser 405	Ser	Ser	Cys	His	Pro 410	Cys	Pro	Pro	Gly	Thr 415	Phe
Ser	Asp	Gly	Thr 420	Lys	Glu	Cys	Arg	Pro 425	Cys	Pro	Ala	Gly	Thr 430	Glu	Pro
Ala	Leu	Gly 435	Phe	Glu	Tyr	Lys	Trp 440	Trp	Asn	Val	Leu	Pro 445	Gly	Asn	Met
Lys	Thr 450	Ser	Cys	Phe	Asn	Val 455	Gly	Asn	Ser	Lys	Cys 460	Asp	Gly	Met	Asn
Gly 465	Trp	Glu	Val	Ala	Gly 470	Asp	His	Ile	Gln	Ser 475	Gly	Ala	Gly	Gly	Ser 480
Asp	Asn	Asp	Tyr	Leu 485	Ile	Leu	Asn	Leu	His 490	Ile	Pro	Gly	Phe	Lys 495	Pro
Pro	Thr	Ser	Met 500	Thr	Gly	Ala	Thr	Gly 505	Ser	Glu	Leu	Gly	Arg 510	Ile	Thr
Phe	Val	Phe 515	Glu	Thr	Leu	Cys	Ser 520	Ala	Asp	Cys	Val	Leu 525	Tyr	Phe	Met
Val	Asp 530	Ile	Asn	Arg	Lys	Ser 535	Thr	Asn	Val	Val	Glu 540	Ser	Trp	Gly	Gly
Thr 545	Lys	Glu	Lys	Gln	Ala 550	Tyr	Thr	His	Ile	Ile 555	Phe	Lys	Asn	Ala	Thr 560
Phe	Thr	Phe	Thr	Trp 565	Ala	Phe	Gln	Arg	Thr 570	Asn	Gln	Gly	Gln	Asp 575	Asn
Arg	Arg	Phe	Ile 580	Asn	Asp	Met	Val	Lys 585	Ile	Tyr	Ser	Ile	Thr 590	Ala	Thr
Asn	Ala	Val 595	Asp	Gly	Val	Ala	Ser 600	Ser	Cys	Arg	Ala	Cys 605	Ala	Leu	Gly
Ser	Glu	Gln	Ser	Gly	Ser	Ser 615	Cys	Val	Pro	Cys	Pro 620	Pro	Gly	His	Tyr
Ile 625	Glu	Lys	Glu	Thr	Asn 630	Gln	Cys	Lys	Glu	Cys 635	Pro	Pro	Asp	Thr	Tyr 640

Leu	Ser	Ile	His	Gln	Val	Tyr	Gly	Lys	Glu	Ala	Cys	Ile	Pro	Cys	Gly
				645					650					655	
Pro	Gly	Ser	Lys	Asn	Asn	Gln	Asp	His	Ser	Val	Cys	Tyr	Ser	Asp	Cys
			660					665					670		
Phe	Phe	Tyr	His	Glu	Lys	Glu	Asn	Gln	Ile	Leu	His	Tyr	Asp	Phe	Ser
		675					680					685			
Asn	Leu	Ser	Ser	Val	Gly	Ser	Leu	Met	Asn	Gly	Pro	Ser	Phe	Thr	Ser
	690					695					700				
Lys	Gly	Thr	Lys	Tyr	Phe	His	Phe	Phe	Asn	Ile	Ser	Leu	Cys	Gly	His
705					710					715					720
Glu	Gly	Lys	Lys	Met	Ala	Leu	Cys	Thr	Asn	Asn	Ile	Thr	Asp	Phe	Thr
				725					730					735	
Val	Lys	Glu	Ile	Val	Ala	Gly	Ser	Asp	Asp	Tyr	Thr	Asn	Leu	Val	Gly
			740					745					750		
Ala	Phe	Val	Cys	Gln	Ser	Thr	Ile	Ile	Pro	Ser	Glu	Ser	Lys	Gly	Phe
		755					760					765			
Arg	Ala	Ala	Leu	Ser	Ser	Gln	Ser	Ile	Ile	Leu	Ala	Asp	Thr	Phe	Ile
	770					775					780				
Gly	Val	Thr	Val	Glu	Thr	Thr	Leu	Lys	Asn	Ile	Asn	Ile	Lys	Glu	Asp
785					790					795					800
Met	Phe	Pro	Val	Pro	Thr	Ser	Gln	Ile	Pro	Asp	Val	His	Phe	Phe	Tyr
				805					810					815	
Lys	Ser	Ser	Thr	Ala	Thr	Thr	Ser	Cys	Ile	Asn	Gly	Arg	Ser	Thr	Ala
			820					825					830		
Val	Lys	Met	Arg	Cys	Asn	Pro	Thr	Lys	Ser	Gly	Ala	Gly	Val	Ile	Ser
		835					840					845			
Val	Pro	Ser	Lys	Cys	Pro	Ala	Gly	Thr	Cys	Asp	Gly	Cys	Thr	Phe	Tyr
	850					855					860				
Phe	Leu	Trp	Glu	Ser	Ala	Glu	Ala	Cys	Pro	Leu	Cys	Thr	Glu	His	Asp
865					870					875					880
Phe	His	Glu	Ile	Glu	Gly	Ala	Cys	Lys	Arg	Gly	Phe	Gln	Glu	Thr	Leu
				885					890					895	

Tyr Val Trp Asn Glu Pro Lys Trp Cys Ile Lys Gly Ile Ser Leu Pro
 900 905 910
 Glu Lys Lys Leu Ala Thr Cys Glu Thr Val Asp Phe Trp Leu Lys Val
 915 920 925
 Gly Ala Gly Val Gly Ala Phe Thr Ala Val Leu Leu Val Ala Leu Thr
 930 935 940
 Cys Tyr Phe Trp Lys Lys Asn Gln Lys Leu Glu Tyr Lys Tyr Ser Lys
 945 950 955 960
 Leu Val Met Thr Thr Asn Ser Lys Glu Cys Glu Leu Pro Ala Ala Asp
 965 970 975
 Ser Cys Ala Ile Met Glu Gly Glu Asp Asn Glu Glu Glu Val Val Tyr
 980 985 990
 Ser Asn Lys Gln Ser Leu Leu Gly Lys Leu Lys Ser Leu Ala Thr Lys
 995 1000 1005
 Glu Lys Glu Asp His Phe Glu Ser Val Gln Leu Lys Thr Ser Arg
 1010 1015 1020
 Ser Pro Asn Ile
 1025
 <210> 5
 <211> 186
 <212> PRT
 <213> human
 <400> 5
 Met Asp Ile Lys Asn Leu Leu Thr Val Cys Thr Ile Phe Tyr Ile Thr
 1 5 10 15
 Thr Leu Ala Thr Ala Asp Ile Pro Thr Ser Ser Leu Pro His Ala Pro
 20 25 30
 Val Asn Gly Ala Cys Asp Glu Gly Glu Tyr Leu Asp Lys Arg His Asn
 35 40 45
 Gln Cys Cys Asn Gln Cys Pro Pro Gly Glu Phe Ala Lys Val Arg Cys
 50 55 60
 Asn Gly Asn Asp Asn Thr Lys Cys Glu Arg Cys Pro Pro His Thr Tyr

65					70						75					80
Thr	Ala	Ile	Pro	Asn	Tyr	Ser	Asn	Gly	Cys	His	Gln	Cys	Arg	Lys	Cys	
				85					90					95		
Pro	Thr	Gly	Ser	Phe	Asp	Lys	Val	Lys	Cys	Thr	Gly	Thr	Gln	Asn	Ser	
			100					105					110			
Lys	Cys	Ser	Cys	Leu	Pro	Gly	Trp	Tyr	Cys	Ala	Thr	Asp	Ser	Ser	Gln	
		115					120					125				
Thr	Glu	Asp	Cys	Arg	Asp	Cys	Ile	Pro	Lys	Arg	Arg	Cys	Pro	Cys	Gly	
	130					135					140					
Tyr	Phe	Gly	Gly	Ile	Asp	Glu	Gln	Gly	Asn	Pro	Ile	Cys	Lys	Ser	Cys	
145					150					155					160	
Cys	Val	Gly	Glu	Tyr	Cys	Asp	Tyr	Leu	Arg	Asn	Tyr	Arg	Leu	Asp	Pro	
				165					170					175		
Phe	Pro	Pro	Cys	Lys	Leu	Ser	Lys	Cys	Asn							
			180					185								

<210> 6
 <211> 277
 <212> PRT
 <213> human

<400> 6

Met	Cys	Val	Gly	Ala	Arg	Arg	Leu	Gly	Arg	Gly	Pro	Cys	Ala	Ala	Leu
1				5					10					15	
Leu	Leu	Leu	Gly	Leu	Gly	Leu	Ser	Thr	Val	Thr	Gly	Leu	His	Cys	Val
			20					25					30		
Gly	Asp	Thr	Tyr	Pro	Ser	Asn	Asp	Arg	Cys	Cys	His	Glu	Cys	Arg	Pro
		35					40					45			
Gly	Asn	Gly	Met	Val	Ser	Arg	Cys	Ser	Arg	Ser	Gln	Asn	Thr	Val	Cys
	50					55					60				
Arg	Pro	Cys	Gly	Pro	Gly	Phe	Tyr	Asn	Asp	Val	Val	Ser	Ser	Lys	Pro
65					70					75					80
Cys	Lys	Pro	Cys	Thr	Trp	Cys	Asn	Leu	Arg	Ser	Gly	Ser	Glu	Arg	Lys
				85					90					95	

Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg Cys Arg Ala Gly
 100 105 110
 Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp Cys Ala Pro Cys
 115 120 125
 Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala Cys Lys Pro Trp
 130 135 140
 Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln Pro Ala Ser Asn
 145 150 155 160
 Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro Ala Thr Gln Pro
 165 170 175
 Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr Val Gln Pro Thr
 180 185 190
 Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr Arg Pro Val Glu
 195 200 205
 Val Pro Gly Gly Arg Ala Val Ala Ala Ile Leu Gly Leu Gly Leu Val
 210 215 220
 Leu Gly Leu Leu Gly Pro Leu Ala Ile Leu Leu Ala Leu Tyr Leu Leu
 225 230 235 240
 Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
 245 250 255
 Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
 260 265 270
 Thr Leu Ala Lys Ile
 275

<210> 7
 <211> 8
 <212> PRT
 <213> human

<400> 7

Pro Cys Gln Glu Lys Asp Tyr His
 1 5

<210> 8
 <211> 8

<212> PRT
<213> human

<400> 8

Gly Lys Glu Cys Thr Phe Ser Cys
1 5

<210> 9
<211> 8
<212> PRT
<213> human

<400> 9

Gly Cys Asn Asn Ser Ser Trp Ile
1 5

<210> 10
<211> 8
<212> PRT
<213> human

<400> 10

Phe Glu Phe Phe Ile Gln Asn Asp
1 5

<210> 11
<211> 8
<212> PRT
<213> human

<400> 11

Gly Ser His Ser Val Met Leu Lys
1 5

<210> 12
<211> 8
<212> PRT
<213> human

<400> 12

Thr Ile Glu Gly Val Ala Tyr Thr
1 5

<210> 13
<211> 8
<212> PRT
<213> human

<400> 13

Ser Gln Phe Ser Gly Ser Ser Glu
1 5

<210> 14
<211> 8
<212> PRT
<213> human

<400> 14

Glu Glu Gly Lys Thr Gln Ile Met
1 5

<210> 15
<211> 8
<212> PRT
<213> human

<400> 15

Asp Gly Thr Lys Glu Cys Arg Pro
1 5

<210> 16
<211> 8
<212> PRT
<213> human

<400> 16

Asp Gly Met Asn Gly Trp Glu Val
1 5

<210> 17
<211> 8
<212> PRT
<213> human

<400> 17

Pro Gly Phe Lys Pro Pro Thr Ser

1 5

<210> 18
<211> 8
<212> PRT
<213> human

<400> 18

Tyr Phe Met Val Asp Ile Asn Arg
1 5

<210> 19
<211> 8
<212> PRT
<213> human

<400> 19

Gln Cys Gln Asp Asn Arg Arg Phe
1 5

<210> 20
<211> 8
<212> PRT
<213> human

<400> 20

Lys Asn Asn Gln Asp His Ser Val
1 5

<210> 21
<211> 8
<212> PRT
<213> human

<400> 21

Cys Gly His Glu Gly Lys Lys Met
1 5

<210> 22
<211> 8
<212> PRT
<213> human

<400> 22

Asp Thr Phe Ile Gly Val Thr Val
1 5

<210> 23
<211> 8
<212> PRT
<213> human

<400> 23

Phe Phe Tyr Lys Ser Ser Thr Ala
1 5

<210> 24
<211> 8
<212> PRT
<213> human

<400> 24

Ile Ser Val Pro Ser Lys Cys Pro
1 5

<210> 25
<211> 8
<212> PRT
<213> human

<400> 25

Arg Gly Phe Gln Glu Thr Leu Tyr
1 5

<210> 26
<211> 8
<212> PRT
<213> human

<400> 26

Lys Asn Gln Lys Lys Lys Lys Thr
1 5

<210> 27
<211> 8
<212> PRT
<213> human

<400> 27

Lys Asn Gln Lys Leu Glu Tyr Lys
1 5

<210> 28
<211> 8
<212> PRT
<213> human

<400> 28

Leu Ala Thr Lys Glu Lys Glu Asp
1 5

<210> 29
<211> 43
<212> PRT
<213> human

<400> 29

Met Ala Pro Trp Asn Val Leu Pro Gly Pro His Phe Pro His Ser Ser
1 5 10 15

Arg Leu His Gly Ser Gly His Ser Arg Leu Ala Ala Ala Ala Ile Ser
20 25 30

Ile Ala Leu Lys Ala Phe Ser Cys Ala Ser Gly
35 40

<210> 30
<211> 9
<212> PRT
<213> human

<400> 30

Thr Ile Glu Glu Glu Gly Ser Ser Glu
1 5

<210> 31
<211> 74
<212> PRT
<213> human

<400> 31

Cys Thr Glu Arg Pro Pro Cys Thr Thr Lys Asp Tyr Phe Gln Ile His
1 5 10 15

Thr Pro Cys Asp Glu Glu Gly Lys Thr Gln Ile Met Tyr Lys Trp Ile
20 25 30

Glu Pro Lys Ile Cys Arg Glu Asp Leu Thr Asp Ala Ile Arg Leu Pro
35 40 45

Pro Ser Gly Glu Lys Lys Asp Cys Pro Pro Cys Asn Pro Gly Phe Tyr
50 55 60

Asn Asn Gly Ser Ser Ser Cys His Pro Cys
65 70

<210> 32
<211> 29
<212> PRT
<213> human

<400> 32

Thr Lys Gly Trp Trp Ile Ile Ser Gly Ser Ser Ser Leu Arg Arg Thr
1 5 10 15

Phe Lys His Ala Phe Cys Ser Thr Phe Ala Ala Glu Cys
20 25

<210> 33
<211> 35
<212> PRT
<213> human

<400> 33

Phe Lys Met Asp Gly Ile Ile Tyr Ser Lys Arg Phe Lys His Ile Thr
1 5 10 15

Ile Val Met Trp Thr Gln Cys Leu Gln Arg Val Trp Thr Gly Met Ile
20 25 30

Lys Pro Pro
35

<210> 34
<211> 37
<212> PRT

<213> human

<400> 34

Gln Asp Asn Arg Pro Ile Pro Pro Leu Ser Ile Ser Ile Val Pro Tyr
 1 5 10 15
 Val Ser Ile Val Ala Gly Leu Ile Leu Trp Ile Ser Ile Asp Val Thr
 20 25 30
 Phe Pro Arg Arg Phe
 35

<210> 35

<211> 78

<212> PRT

<213> human

<400> 35

Lys Asn Gln Lys Leu Glu Tyr Lys Tyr Ser Lys Leu Val Met Thr Thr
 1 5 10 15
 Asn Ser Lys Glu Cys Glu Leu Pro Ala Ala Asp Ser Cys Ala Ile Met
 20 25 30
 Glu Gly Glu Asp Asn Glu Glu Glu Val Val Tyr Ser Asn Lys Gln Ser
 35 40 45
 Leu Leu Gly Lys Leu Lys Ser Leu Ala Thr Lys Glu Lys Glu Asp His
 50 55 60
 Phe Glu Ser Val Gln Leu Lys Thr Ser Arg Ser Pro Asn Ile
 65 70 75

<210> 36

<211> 46

<212> DNA

<213> human

<400> 36

gcagcacata tgggggacct gccctcctcc tccagccgcc cgcttc
 46

<210> 37

<211> 46

<212> DNA

<213> human

<400> 37

gcagcaacta gtttagtcaa ccgtttcaca ggttgccaac tttttc
46

<210> 38

<211> 42

<212> DNA

<213> human

<400> 38

gcagcaggta cctcatatat ttggggatct tgaggttttc ag
42

<210> 39

<211> 48

<212> DNA

<213> human

<400> 39

gcagcaagat ctccgccatc atgctgttcc gcgcccgggg gccggtac
48

<210> 40

<211> 27

<212> DNA

<213> human

<400> 40

gcagcacata tgctgttccg cgcccgg
27

<210> 41

<211> 59

<212> DNA

<213> human

<400> 41

cgcaactagtt caagcgtagt ctgggacgtc gtatgggtag ttgaacagat tcaaaatgg
59

<210> 42

<211> 733
<212> DNA
<213> human

<400> 42
gggatccgga gcccaaattct tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg
60
aattcgaggg tgcaccgtca gtcttcctct tccccccaaa acccaaggac accctcatga
120
tctcccggac tcctgaggtc acatgcgtgg tgggtggacgt aagccacgaa gaccctgagg
180
tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg
240
aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact
300
ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca acccccatcg
360
agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc
420
catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctgggc aaaggcttct
480
atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagAAC aactacaaga
540
ccacgcctcc cgtgctggac tccgacggct ccttcttctt ctacagcaag ctcaccgtgg
600
acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc
660
acaaccacta cacgcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc
720
gactctagag gat
733

<210> 43
<211> 464
<212> PRT

<213> human

<400> 43

Met	Lys	Asn	Gln	Val	Cys	Ser	Lys	Cys	Gly	Glu	Gly	Thr	Tyr	Ser	Leu	1	5	10	15
Gly	Ser	Gly	Ile	Lys	Phe	Asp	Glu	Trp	Asp	Glu	Leu	Pro	Ala	Gly	Phe	20	25	30	
Ser	Asn	Ile	Ala	Thr	Phe	Met	Asp	Thr	Val	Val	Gly	Pro	Ser	Asp	Ser	35	40	45	
Arg	Pro	Asp	Gly	Cys	Asn	Asn	Ser	Ser	Trp	Ile	Pro	Arg	Gly	Asn	Tyr	50	55	60	
Ile	Glu	Ser	Asn	Arg	Asp	Asp	Cys	Thr	Val	Ser	Leu	Ile	Tyr	Ala	Val	65	70	75	80
His	Leu	Lys	Lys	Ser	Gly	Tyr	Val	Phe	Phe	Glu	Tyr	Gln	Tyr	Val	Asp	85	90	95	
Asn	Asn	Ile	Phe	Phe	Glu	Phe	Phe	Ile	Gln	Asn	Asp	Gln	Cys	Gln	Glu	100	105	110	
Met	Asp	Thr	Thr	Thr	Asp	Lys	Trp	Val	Lys	Leu	Thr	Asp	Asn	Gly	Glu	115	120	125	
Trp	Gly	Ser	His	Ser	Val	Met	Leu	Lys	Ser	Gly	Thr	Asn	Ile	Leu	Tyr	130	135	140	
Trp	Arg	Thr	Thr	Gly	Ile	Leu	Met	Gly	Ser	Lys	Ala	Val	Lys	Pro	Val	145	150	155	160
Leu	Val	Lys	Asn	Ile	Thr	Ile	Glu	Gly	Val	Ala	Tyr	Thr	Ser	Glu	Cys	165	170	175	
Phe	Pro	Cys	Lys	Pro	Gly	Thr	Phe	Ser	Asn	Lys	Pro	Gly	Ser	Phe	Asn	180	185	190	
Cys	Gln	Val	Cys	Pro	Arg	Asn	Thr	Tyr	Ser	Glu	Lys	Gly	Ala	Lys	Glu	195	200	205	
Cys	Ile	Arg	Cys	Lys	Asp	Asp	Ser	Gln	Phe	Ser	Glu	Glu	Gly	Ser	Ser	210	215	220	
Glu	Cys	Thr	Glu	Arg	Pro	Pro	Cys	Thr	Thr	Lys	Asp	Tyr	Phe	Gln	Ile	225	230	235	240

His	Thr	Pro	Cys	Asp	Glu	Glu	Gly	Lys	Thr	Gln	Ile	Met	Tyr	Lys	Trp
				245					250					255	
Ile	Glu	Pro	Lys	Ile	Cys	Arg	Glu	Asp	Leu	Thr	Asp	Ala	Ile	Arg	Leu
			260					265					270		
Pro	Pro	Ser	Gly	Glu	Lys	Lys	Asp	Cys	Pro	Pro	Cys	Asn	Pro	Gly	Phe
		275					280					285			
Tyr	Asn	Asn	Gly	Ser	Ser	Ser	Cys	His	Pro	Cys	Pro	Pro	Gly	Thr	Phe
	290					295					300				
Ser	Asp	Gly	Thr	Lys	Glu	Cys	Arg	Pro	Cys	Pro	Ala	Gly	Thr	Glu	Pro
305					310					315					320
Ala	Leu	Gly	Phe	Glu	Tyr	Lys	Trp	Trp	Asn	Val	Leu	Pro	Gly	Asn	Met
				325					330					335	
Lys	Thr	Ser	Cys	Phe	Asn	Val	Gly	Asn	Ser	Lys	Cys	Asp	Gly	Met	Asn
			340					345					350		
Gly	Trp	Glu	Val	Ala	Gly	Asp	His	Ile	Gln	Ser	Gly	Ala	Gly	Gly	Ser
		355					360					365			
Asp	Asn	Asp	Tyr	Leu	Ile	Leu	Asn	Leu	His	Ile	Pro	Gly	Phe	Lys	Pro
	370					375					380				
Pro	Thr	Ser	Met	Thr	Gly	Ala	Thr	Gly	Ser	Glu	Leu	Gly	Arg	Ile	Thr
385					390					395					400
Phe	Val	Phe	Glu	Thr	Leu	Cys	Ser	Ala	Asp	Cys	Val	Leu	Tyr	Phe	Met
				405					410					415	
Val	Asp	Ile	Asn	Arg	Lys	Ser	Thr	Asn	Val	Val	Glu	Ser	Trp	Gly	Gly
			420					425					430		
Thr	Lys	Glu	Lys	Gln	Ala	Tyr	Thr	His	Ile	Ile	Phe	Lys	Asn	Ala	Thr
		435					440					445			
Phe	Thr	Phe	Thr	Trp	Gly	Ile	Pro	Arg	Glu	Leu	Ile	Gln	Gly	Pro	Arg
	450					455					460				